

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 3, 2003, 15:02:13 ; Search time 83 seconds
(without alignments)
593.316 Million cell updates/sec

Title: US-09-887-784-4
Perfect score: 1274

Sequence: 1 MYSKGEELFTGVVPILVELD.....VLLGFVTAAGITLGMDELXK 239

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriaph:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1240	97.3	238	5 Q93125	Q93125 aequorea vi
2	1239	97.3	238	5 Q27903	Q27903 unidentified
3	1227	96.3	758	4 Q963Q1	Q963Q1 homo sapien
4	1205	94.6	238	5 Q17105	Q17105 aequorea vi
5	1190	93.4	238	5 Q17106	Q17106 aequorea vi
6	1085	85.2	238	5 Q8WTC6	Q8WTC6 aequorea ma
7	1081	84.9	238	5 Q8WP95	Q8WP95 aequorea ma
8	1077	84.5	238	5 Q8WTC4	Q8WTC4 aequorea ma
9	1075	84.4	238	5 Q8WTD0	Q8WTD0 aequorea ma
10	1074	84.3	238	5 Q8WTC9	Q8WTC9 aequorea ma
11	1074	84.3	238	5 Q8WTC8	Q8WTC8 aequorea ma
12	1072	84.1	238	5 Q8WTC7	Q8WTC7 aequorea ma
13	1070	84.0	238	5 Q8WTC5	Q8WTC5 aequorea ma
14	252.5	19.8	225	5 Q95UA7	Q95UA7 montastraea
15	247	19.4	225	5 Q963F5	Q963F5 montastraea
16	244.5	19.2	236	5 Q8T6U0	Q8T6U0 dendroneph

17	238.5	18.7	266	5 Q9U6Y3	Q9U6Y3 clavularia
18	232	18.2	225	5 Q8T5F1	Q8T5F1 montastraea
19	209	16.4	234	5 Q8T5F2	Q8T5F2 montastraea
20	208.5	16.4	229	5 Q9U6Y6	Q9U6Y6 anemonia ma
21	206	16.2	227	5 Q963P9	Q963P9 montastraea
22	205.5	16.1	232	5 Q9GP15	Q9GP15 anemonia su
23	204	16.0	221	5 Q95P04	Q95P04 gonioptora t
24	203.5	16.0	238	5 Q9BLY9	Q9BLY9 renilla mue
25	202	15.9	227	5 Q95VT0	Q95VT0 montastraea
26	201.5	15.8	225	5 Q9U6Y8	Q9U6Y8 discosoma s
27	201.5	15.8	232	5 Q9GZ28	Q9GZ28 anemonia su
28	198.5	15.6	225	5 Q8T6T9	Q8T6T9 heteractis
29	198	15.5	235	5 Q8T5F0	Q8T5F0 scolymlia cu
30	197.5	15.5	232	5 Q9U6Y7	Q9U6Y7 discosoma s
31	188.5	14.8	227	5 Q95W85	Q95W85 heteractis
32	187.5	14.7	228	5 Q9GP16	Q9GP16 anemonia su
33	187	14.7	230	5 Q9GTJ7	Q9GTJ7 discosoma s
34	184.5	14.5	233	5 Q963I9	Q963I9 renilla ren
35	183.5	14.4	238	5 Q9BLZ0	Q9BLZ0 ptilosarcus
36	180.5	14.2	227	5 Q95W86	Q95W86 condylactis
37	174.5	13.7	227	5 Q95W11	Q95W11 condylactis
38	172.5	13.5	231	5 Q9U6Y5	Q9U6Y5 zoanthus sp
39	170.5	13.4	229	5 Q8T5E7	Q8T5E7 condylactis
40	168.5	13.2	231	5 Q8T5E8	Q8T5E8 ricordea fl
41	166	13.0	231	5 Q9U6Y4	Q9U6Y4 zoanthus sp
42	161	12.6	234	5 Q8T5F3	Q8T5F3 scolymlia cu
43	158.5	12.4	231	5 Q8T4U4	Q8T4U4 zoanthus sp
44	150	11.8	231	5 Q8T5T8	Q8T5T8 discosoma s
45	143	11.2	231	5 Q8T5E9	Q8T5E9 ricordea fl

ALIGNMENTS

RESULT 1

ID	Q93125	PRELIMINARY;	PRT;	238 AA.
AC	Q93125;			
DT	01-FEB-1997 (TrEMBLrel. 02, Created)			
DT	01-FEB-1997 (TrEMBLrel. 02, Last sequence update)			
DT	01-JUN-2002 (TrEMBLrel. 21, Last annotation update)			
DE	Green fluorescent protein mutant 3.			
GN	GFP.			
OS	Aequorea victoria (Jellyfish).			
OC	Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydrozoa; Leptomedusae;			
OC	Aequoreidae; Aequorea.			
OX	NCBI_TaxID=6100;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RP	MEDLINE=96305137; PubMed=8707053;			
RA	Cormack B.P., Valdivia R.H., Falkow S.;			
RT	*FACS-optimized mutants of the green fluorescent protein (GFP).*			
RL	Gene 173:33-38(1996).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RA	Cormack B.P., Bertram G., Egerton M., Gow N.A.R., Falkow S.,			
RA	Brown A.J.P.;			
RT	*Feast Enhanced Green Fluorescent Protein (yEGFP): a reporter of gene			
RL	expression in Candida albicans.*;			
RL	Microbiology 0:0-0(1996).			
DR	EMBL; U73901; AAB18957.1; -.			
DR	HSSP; P42212; 1BFP.			
DR	InterPro; IPR000786; Green_fl_protein.			
DR	Pfam; PF01353; GFP; 1.			
DR	PRINTS; PR01229; GFP; 1.			
DR	PRODOM; PD013756; Green_fl_protein; 1.			
SQ	SEQUENCE 238 AA; 26840 MW; A28622809A9DEA60 CRC64;			

Query Match 97.3%; Score 1240; DB 5; Length 238;
Best Local Similarity 97.5%; Pred. No. 1.3e-94;
Matches 232; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
QY 2 VSKGEELFTGVVPILVELDGVNGHKFSVSGEGDATYGLKFLRFTCTTGKLPVWPPTL 61

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Db 1 MKGGEELFTGVVPIVLVDGDNVNGHKFSVSGEGDATYGLKTLKFICTTGKLPVWPPTL 60
QY 62 VTTLSYGVQCFSRYPDMKQHDFFKFSAMPEGYVQERTIFFKDDGNKTRAEVKEGDTLV 121
Db 61 VTTFGYGVQCFARYPDMKQHDFFKFSAMPEGYVQERTIFFKDDGNKTRAEVKEGDTLV 120
QY 122 NRIELKGIDFKEDGNLGHKLEYNHSHVYIMADKQKNGIKYKFKIRHNIEDGSVOLAD 181
Db 121 NRIELKGIDFKEDGNLGHKLEYNHSHVYIMADKQKNGIKYKFKIRHNIEDGSVOLAD 180
QY 182 HYQONTPIGDGPVLLPDNHYLSTQSALSADPNKRDHMLGVTAAGITLGMDELK 239
Db 181 HYQONTPIGDGPVLLPDNHYLSTQSALSADPNKRDHMLGVTAAGITLGMDELK 238

RESULT 2
Q27903 PRELIMINARY: PRT: 238 AA.
ID Q27903;
AC Q27903;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Green fluorescent protein.
GN GFP.
OS unidentified.
OC unclassified.
ON NCBI_TaxID=32644;
RX SEQUENCE FROM N.A.
RP MEDLINE=97299832; PubMed=9154981;
RA Rouwendal G.J.A., Mendes O., Wolbert E.J.H., de Boer A.D.;
RT "Enhanced expression in tobacco of the gene encoding green fluorescent
RL Plant Mol. Biol. 33:989-999(1997).
DR EMBL; X96418; CAA65278.1; -
DR HSP; P42212; IGFL.
DR InterPro; IPR000786; Green_fl_protein.
DR Pfam; PF01353; GFP; 1.
DR PRINTS; PR01229; GFP.
DR ProDom; PD013756; Green_fl_protein; 1.
SQ SEQUENCE 238 AA; 26884 MW; CA932D47262AF2D3 CRC64;

Query Match 97.3%; Score 1239; DB 5; Length 238;
Best Local Similarity 97.5%; Pred. No. 1.5e-94;
Matches 232; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 VSKGEELFTGVVPIVLVDGDNVNGHKFSVSGEGDATYGLKTLKFICTTGKLPVWPPTL 61
Db 1 MKGGEELFTGVVPIVLVDGDNVNGHKFSVSGEGDATYGLKTLKFICTTGKLPVWPPTL 60
QY 62 VTTLSYGVQCFSRYPDMKQHDFFKFSAMPEGYVQERTIFFKDDGNKTRAEVKEGDTLV 121
Db 61 VTTFSYGVQCFSRYPDMKQHDFFKFSAMPEGYVQERTIFFKDDGNKTRAEVKEGDTLV 120
QY 122 NRIELKGIDFKEDGNLGHKLEYNHSHVYIMADKQKNGIKYKFKIRHNIEDGSVOLAD 181
Db 121 NRIELKGIDFKEDGNLGHKLEYNHSHVYIMADKQKNGIKYKFKIRHNIEDGSVOLAD 180
QY 182 HYQONTPIGDGPVLLPDNHYLSTQSALSADPNKRDHMLGVTAAGITLGMDELK 239
Db 181 HYQONTPIGDGPVLLPDNHYLSTQSALSADPNKRDHMLGVTAAGITLGMDELK 238

RESULT 3
Q96JQ1 PRELIMINARY: PRT: 758 AA.
ID Q96JQ1;
AC Q96JQ1;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Raichu404X.
GN RAICHU404X.

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OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
ON NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=SPLEEN;
RX MEDLINE=21322811; PubMed=11429608;
RA Mochizuki N., Yamashita S., Kurokawa K., Ohba Y., Nagai T.,
RA Miyawaki A., Matsuda M.;
RT "Spacio-temporal Images of Growth Factor-induced Activation of Ras and
RT Rap1.";
RL Nature 411:1065-1068(2001).
DR EMBL; AB051846; BAB61868.1; -
DR InterPro; IPR000786; Green_fl_protein.
DR InterPro; IPR001230; Prenyl_site.
DR InterPro; IPR001806; Ras_trnsmfmg.
DR InterPro; IPR003116; RBD.
DR InterPro; IPR005225; Small_GTP.
DR Pfam; PF01353; GFP; 2.
DR Pfam; PF02196; RBD; 1.
DR Pfam; PF02196; RBD; 1.
DR ProDom; PD013756; Green_fl_protein; 2.
DR TIGRFAMs; TIGR00231; small_GTP; 1.
DR PROSITE; PS00294; PRENYLATION; UNKNOWN_1.
KW GTP-binding.
SQ SEQUENCE 758 AA; 85015 MW; 8612408F607CFD49 CRC64;

Query Match 96.3%; Score 1227; DB 4; Length 758;
Best Local Similarity 97.5%; Pred. No. 6.9e-93;
Matches 231; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 MVSKEELFTGVVPIVLVDGDNVNGHKFSVSGEGDATYGLKTLKFICTTGKLPVWPPT 60
Db 498 MVSKEELFTGVVPIVLVDGDNVNGHKFSVSGEGDATYGLKTLKFICTTGKLPVWPPT 557
QY 61 LVTTLSYGVQCFSRYPDMKQHDFFKFSAMPEGYVQERTIFFKDDGNKTRAEVKEGDTLV 120
Db 558 LVTTLTGWQCFSRYPDMKQHDFFKFSAMPEGYVQERTIFFKDDGNKTRAEVKEGDTLV 617
QY 121 VNRIELKGIDFKEDGNLGHKLEYNHSHVYIMADKQKNGIKYKFKIRHNIEDGSVOL 180
Db 618 VNRIELKGIDFKEDGNLGHKLEYNHSHVYIMADKQKNGIKYKFKIRHNIEDGSVOL 677
QY 181 DHYQONTPIGDGPVLLPDNHYLSTQSALSADPNKRDHMLGVTAAGITLGMDEL 237
Db 678 DHYQONTPIGDGPVLLPDNHYLSTQSALSADPNKRDHMLGVTAAGITLGMDEL 734

RESULT 4
Q17105 PRELIMINARY: PRT: 238 AA.
ID Q17105;
AC Q17105;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Green fluorescent protein (Fragment).
GN GFP.
OS Aequorea victoria (Jellyfish).
OC Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroidea; Leptomedusae;
OC Aequoreidae; Aequorea.
ON NCBI_TaxID=6100;
RN [1]
RP SEQUENCE FROM N.A.
RA Watkins J.N., Campbell A.K.;
RL Submitted (JAN-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; X83959; CAA58789.1; -
DR HSP; P42212; IGFL.
DR InterPro; IPR000786; Green_fl_protein.
DR Pfam; PF01353; GFP; 1.
DR PRINTS; PR01229; GFP.
DR ProDom; PD013756; Green_fl_protein; 1.
NON_TER 238 238

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SQ SEQUENCE 238 AA; 26950 MW; 26E2BE450E748B44 CRC64;
Query Match 94.6%; Score 1205; DB 5; Length 238;
Best Local Similarity 94.1%; Pred. No. 9.8e-92;
Matches 224; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 2 VSKGEELFTGVVPIVLVDGVDYNGHKFSVSGEGDATYKGLTKFKICTTGKLPVWPPTL 61
DB 1 MSKGEELFTGVVPIVLVDGVDYNGKFSVSGEGDATYKGLTKFKICTTGKLPVWPPTL 60
QY 62 VTTLSYGVCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 121
DB 61 VTTLSYGVCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 120
QY 122 NRIELKGIDFKEDGNILGHKLEYNNSHNYIMADKQKNGIKVNFKIRHNIEDGSVOLAD 181
DB 121 NRIELKGIDFKEDGNILGHKLEYNNSHNYIMADKQKNGIKVNFKIRHNIEDGSVOLAD 180
QY 182 HYQONTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMLVLLGFVTAAGITLGMDELYK 239
DB 181 HYQONTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMLVLLGFVTAAGITLGMDELYK 238

RESULT 5
Q17106 PRELIMINARY; PRT; 238 AA.
AC Q17106
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Green fluorescent protein (Fragment).
GN GFP.
OS Aequorea victoria (Jellyfish).
OC Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
OC Aequoreidae; Aequorea.
OX NCBI_TaxID=6100;
RN [1]
RA Watkins J.N., Campbell A.K.;
RL Submitted (JAN-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; X83960; CAA58790.1; -.
DR HSSP; P42212; 1BFP.
DR InterPro; IPR000786; Green_fl_protein.
DR Pfam; PF01353; GFP; 1.
DR ProDom; PD013756; Green_fl_protein; 1.
FT NON_TER 238
SQ SEQUENCE 238 AA; 26867 MW; BD4648262D8EABD4 CRC64;

Query Match 93.4%; Score 1190; DB 5; Length 238;
Best Local Similarity 93.3%; Pred. No. 1.7e-90;
Matches 222; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 2 VSKGEELFTGVVPIVLVDGVDYNGHKFSVSGEGDATYKGLTKFKICTTGKLPVWPPTL 61
DB 1 MSKGEELFTGVVPIVLVDGVDYNGKFSVSGEGDATYKGLTKFKICTTGKLPVWPPTL 60
QY 62 VTTLSYGVCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 121
DB 61 VTTLSYGVCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 120
QY 122 NRIELKGIDFKEDGNILGHKLEYNNSHNYIMADKQKNGIKVNFKIRHNIEDGSVOLAD 181
DB 121 NRIELKGIDFKEDGNILGHKLEYNNSHNYIMADKQKNGIKVNFKIRHNIEDGSVOLAD 180
QY 182 HYQONTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMLVLLGFVTAAGITLGMDELYK 239
DB 181 HYQONTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMLVLLGFVTAAGITLGMDELYK 238

RESULT 6
Q8WTC6 PRELIMINARY; PRT; 238 AA.
ID Q8WTC6
Query Match 84.9%; Score 1081; DB 5; Length 238;
Best Local Similarity 81.9%; Pred. No. 1.7e-81;
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Q8WTC6;
01-MAR-2002 (TREMBlrel. 20, Created)
01-MAR-2002 (TREMBlrel. 20, Last sequence update)
01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Green fluorescent protein.
GN GFP.
OS Aequorea macrodactyla.
OC Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
OC Aequoreidae; Aequorea.
OX NCBI_TaxID=147615;
RN [1]
RA Luo W.X., Zhang J., Yang H.J., Xie X.Y., Li S.W., Guan B.Q., Chen M.,
Li S.J., Xi N.S.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF435431; AAL33916.1; -.
DR InterPro; IPR000786; Green_fl_protein.
DR Pfam; PF01353; GFP; 1.
DR ProDom; PD013756; Green_fl_protein; 1.
SQ SEQUENCE 238 AA; 27015 MW; 6B8FD75E88926903 CRC64;

Query Match 85.2%; Score 1085; DB 5; Length 238;
Best Local Similarity 82.4%; Pred. No. 7.9e-82;
Matches 196; Conservative 20; Mismatches 22; Indels 0; Gaps 0;

QY 2 VSKGEELFTGVVPIVLVDGVDYNGHKFSVSGEGDATYKGLTKFKICTTGKLPVWPPTL 61
DB 1 MSKGEELFTGVVPIVLVDGVDYNGKFSVSGEGDATYKGLTKFKICTTGKLPVWPPTL 60
QY 62 VTTLSYGVCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 121
DB 61 VTTLSYGVCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 120
QY 122 NRIELKGIDFKEDGNILGHKLEYNNSHNYIMADKQKNGIKVNFKIRHNIEDGSVOLAD 181
DB 121 NRIELKGIDFKEDGNILGHKLEYNNSHNYIMADKQKNGIKVNFKIRHNIEDGSVOLAD 180
QY 182 HYQONTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMLVLLGFVTAAGITLGMDELYK 239
DB 181 HYQONTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMLVLLGFVTAAGITLGMDELYK 238

RESULT 7
Q8WP95 PRELIMINARY; PRT; 238 AA.
ID Q8WP95
AC Q8WP95;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Green fluorescent protein.
GN GFPXM.
OS Aequorea macrodactyla.
OC Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
OC Aequoreidae; Aequorea.
OX NCBI_TaxID=147615;
RN [1]
RA Luo W.X., Zhang J., Yang H.J., Xie X.Y., Li S.W., Qin Y.X., Pang S.Q.,
Li S.J., Xia N.S.;
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY013824; AAK02062.1; -.
DR EMBL; AY013821; AAK02059.1; -.
DR InterPro; IPR000786; Green_fl_protein.
DR Pfam; PF01353; GFP; 1.
DR ProDom; PD013756; Green_fl_protein; 1.
SQ SEQUENCE 238 AA; 27049 MW; 8185D0E5E529012B CRC64;

Query Match 84.9%; Score 1081; DB 5; Length 238;
Best Local Similarity 81.9%; Pred. No. 1.7e-81;
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Matches 195; Conservative 20; Mismatches 23; Indels 0; Gaps 0;

QY 2 VSKGELFTGVVPIVLVDGVDVNGHKFSVSGEGDGYGKLTLEICTTGKLPVWPPTL 61
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 1 MSKGEELFTGIVPVLIELDGDVGHGKFSVRGEGDADYKLEIKFICTTGKLPVWPPTL 60
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 QY 62 VTTLSYGVOCFSRYPDHMKQHDFFKFSAMPEGVVQERTIFFKDDGNTKTRAEVKEGDTLV 121
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 61 VTTFSYGTCFARYPEHMKMNDFFKFSAMPEGVVQERTIFFQDDGKTKRGEVKEGDTLV 120
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 QY 122 NRIELKGIDFKEDGNILGHKLEYNNSHNYIMADKQNGIKVNFIRINIEDGSVOLAD 181
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 121 NRIELKGIDFKEDGNILGHKLEYNNSHNYIMADKQNGIKVNFIRINIEDGSVOLAD 180
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 QY 182 HYQONTPTGDPVLLPDNHYLSTQALSADKDPNEKRDHNVLLGFVTAAGITLGMDELYK 239
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 181 HYQTNVPLDGPVLIPINHYLSTQALSADKDRNETHRVNLFEEFSACGTHGMDELYK 238
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 8
 Q8WTC4 PRELIMINARY; PRT; 238 AA.
 AC Q8WTC4: 01-MAR-2002 (TremBLrel. 20, Created)
 DT 01-MAR-2002 (TremBLrel. 20, Last sequence update)
 DE Green fluorescent protein.
 GN GFP.
 OS Aequorea macrodactyla.
 OC Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydrozoa; Leptomedusae;
 OX NCBI_TaxID=147615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SHG24;
 RA Luo W.X., Zhang J., Yang H.J., Xie X.Y., Li S.W., Guan B.Q., Chen M.,
 Li S.J., Xia N.S.;
 RT "Colorful mutants of green fluorescent protein from Aequorea
 macrodactyla.";
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF435433; AAL33912.1;
 DR InterPro; IPR000786; Green_fl_protein.
 DR Pfam; PF01353; GFP; 1.
 DR ProDom; PD013756; Green_fl_protein; 1.
 DR ProDom; PD013756; Green_fl_protein; 1.
 SQ SEQUENCE 238 AA; 26956 MW; 75521EAF0CEBA73A CRC64;

Query Match 84.5%; Score 1077; DB 5; Length 238;
 Best Local Similarity 82.8%; Pred. No. 3.6e-81;
 Matches 197; Conservative 17; Mismatches 24; Indels 0; Gaps 0;

QY 2 VSKGELFTGVVPIVLVDGVDVNGHKFSVSGEGDGYGKLTLEICTTGKLPVWPPTL 61
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 1 MSKGEELFTGVVPIVLVDGVDVNGHKFSVRGEGDADYKLEIKFICTTGKLPVWPPTL 60
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 QY 62 VTTLSYGVOCFSRYPDHMKQHDFFKFSAMPEGVVQERTIFFKDDGNTKTRAEVKEGDTLV 121
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 61 VTTLSYGTCFARYPEHMKMNDFFKFSAMPEGVVQERTIFFQDDGKTKRGEVKEGDTLV 120
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 QY 122 NRIELKGIDFKEDGNILGHKLEYNNSHNYIMADKQNGIKVNFIRINIEDGSVOLAD 181
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 121 NRIELKGIDFKEDGNILGHKLEYNNSHNYIMADKQNGIKVNFIRINIEDGSVOLAD 180
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 QY 182 HYQONTPTGDPVLLPDNHYLSTQALSADKDPNEKRDHNVLLGFVTAAGITLGMDELYK 239
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 181 HYQTNVPLDGPVLIPINHYLSTQALSADKDRNETHRVNLFEEFSACGTHGMDELYK 238
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 9
 Q8WTD0 PRELIMINARY; PRT; 238 AA.
 AC Q8WTD0: 01-MAR-2002 (TremBLrel. 20, Created)
 DT 01-MAR-2002 (TremBLrel. 20, Last sequence update)

DT 01-JUN-2002 (TremBLrel. 21, Last annotation update)
 DE Green fluorescent protein.
 GN GFP.
 OS Aequorea macrodactyla.
 OC Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydrozoa; Leptomedusae;
 OX NCBI_TaxID=147615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=GFPX161;
 RA Luo W.X., Zhang J., Yang H.J., Xie X.Y., Li S.W., Guan B.Q., Chen M.,
 Li S.J., Xia N.S.;
 RT "Colorful mutants of green fluorescent protein from Aequorea
 macrodactyla.";
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF435427; AAL33912.1;
 DR InterPro; IPR000786; Green_fl_protein.
 DR Pfam; PF01353; GFP; 1.
 DR ProDom; PD013756; Green_fl_protein; 1.
 DR ProDom; PD013756; Green_fl_protein; 1.
 SQ SEQUENCE 238 AA; 26997 MW; 5F80A192173CB84D CRC64;

Query Match 84.4%; Score 1075; DB 5; Length 238;
 Best Local Similarity 81.5%; Pred. No. 5.3e-81;
 Matches 194; Conservative 20; Mismatches 24; Indels 0; Gaps 0;

QY 2 VSKGEELFTGVVPIVLVDGVDVNGHKFSVSGEGDGYGKLTLEICTTGKLPVWPPTL 61
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 1 MSKGEELFTGIVPVLIELDGDVGHGKFSVRGEGDADYKLEIKFICTTGKLPVWPPTL 60
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 QY 62 VTTLSYGVOCFSRYPDHMKQHDFFKFSAMPEGVVQERTIFFKDDGNTKTRAEVKEGDTLV 121
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 61 VTTLSYGTCFARYPEHMKMNDFFKFSAMPEGVVQERTIFFQDDGKTKRGEVKEGDTLV 120
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 QY 122 NRIELKGIDFKEDGNILGHKLEYNNSHNYIMADKQNGIKVNFIRINIEDGSVOLAD 181
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 121 NRIELKGIDFKEDGNILGHKLEYNNSHNYIMADKQNGIKVNFIRINIEDGSVOLAD 180
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 QY 182 HYQONTPTGDPVLLPDNHYLSTQALSADKDPNEKRDHNVLLGFVTAAGITLGMDELYK 239
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 181 HYQTNVPLDGPVLIPINHYLSTQALSADKDRNETHRVNLFEEFSACGTHGMDELYK 238
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 10
 Q8WTC9 PRELIMINARY; PRT; 238 AA.
 AC Q8WTC9: 01-MAR-2002 (TremBLrel. 20, Created)
 DT 01-MAR-2002 (TremBLrel. 20, Last sequence update)
 DE Green fluorescent protein.
 GN GFP.
 OS Aequorea macrodactyla.
 OC Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydrozoa; Leptomedusae;
 OX NCBI_TaxID=147615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=GFPX162;
 RA Luo W.X., Zhang J., Yang H.J., Xie X.Y., Li S.W., Guan B.Q., Chen M.,
 Li S.J., Xia N.S.;
 RT "Colorful mutants of green fluorescent protein from Aequorea
 macrodactyla.";
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF435428; AAL33913.1;
 DR InterPro; IPR000786; Green_fl_protein.
 DR Pfam; PF01353; GFP; 1.
 DR ProDom; PD013756; Green_fl_protein; 1.
 DR ProDom; PD013756; Green_fl_protein; 1.
 SQ SEQUENCE 238 AA; 27031 MW; 5F80A19C19DC584D CRC64;

Query Match 84.3%; Score 1074; DB 5; Length 238;
 Best Local Similarity 81.5%; Pred. No. 6.4e-81;
 Matches 194; Conservative 20; Mismatches 24; Indels 0; Gaps 0;

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QY 2 VSKGEELFTGVVPIVLVDGVDVNGHKFSVSGEGEDATYKLTGKLFICTTGKLPVWPPTL 61
Db 1 MSKGEELFTGIVPVLIELDGDVGHGKFSVRGEGDADYKLEIKFICTTGKLPVWPPTL 60
QY 62 VTTLSYGVOCSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNKTKRAEVKFGDTLV 121
Db 61 VTTLGYGIOCFARYPEHKMNDFFKSAMPEGYIQERTIFFQDDGKYKTRGEVKEGDTLV 120
QY 122 NRIELKGIDFKEDGNILGHKLEYNHNYSVIMADKQNGIKVNFKIRHNIEDGSGVOLAD 181
Db 121 NRIELKGMDFKEDGNILGHKLEYNHNYSVIMADKQNGIKVNFKIRHNIEGGGVQVLAD 180
QY 182 HYQONTPIGDGPVLLPDNHYLSQTALSADKPNKRDHMLVGLGVTAAAGITLGMDELYK 239
Db 181 HYQTNVPLDGPVLLIPINHYLSQTALSKDRNETRDHMLVLEFFSACGHTHGMDLYK 238

RESULT 11
Q8WTC8 PRELIMINARY; PRT; 238 AA.
AC Q8WTC8;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DE 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Green fluorescent protein.
OS Aequorea macrodactyla.
OC Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
OC Aequoreidae; Aequorea.
OX NCBI_TaxID=147615;
RN [1]
RA Luo W.X., Zhang J., Yang H.J., Xie X.Y., Li S.W., Guan B.Q., Chen M.,
Li S.J., Xia N.S.;
RT "Colorful mutants of green fluorescent protein from Aequorea
macrodactyla."
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF435429; AAL33914.1; -
DR InterPro; IPR000786; Green_fl_protein.
DR Pfam; PF01353; GFP; 1.
DR ProDom; PD013756; Green_fl_protein; 1.
SQ SEQUENCE 238 AA; 27047 MW; 5F80A18FA1E7C84D CRC64;

Query Match 84.3%; Score 1074; DB 5; Length 238;
Best Local Similarity 81.5%; Pred. No. 6.4e-81;
Matches 194; Conservative 20; Mismatches 24; Indels 0; Gaps 0;

QY 2 VSKGEELFTGVVPIVLVDGVDVNGHKFSVSGEGEDATYKLTGKLFICTTGKLPVWPPTL 61
Db 1 MSKGEELFTGIVPVLIELDGDVGHGKFSVRGEGDADYKLEIKFICTTGKLPVWPPTL 60
QY 62 VTTLSYGVOCSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNKTKRAEVKFGDTLV 121
Db 61 VTTLGYGIOCFARYPEHKMNDFFKSAMPEGYIQERTIFFQDDGKYKTRGEVKEGDTLV 120
QY 122 NRIELKGIDFKEDGNILGHKLEYNHNYSVIMADKQNGIKVNFKIRHNIEDGSGVOLAD 181
Db 121 NRIELKGMDFKEDGNILGHKLEYNHNYSVIMADKQNGIKVNFKIRHNIEGGGVQVLAD 180
QY 182 HYQONTPIGDGPVLLPDNHYLSQTALSADKPNKRDHMLVGLGVTAAAGITLGMDELYK 239
Db 181 HYQTNVPLDGPVLLIPINHYLSQTALSKDRNETRDHMLVLEFFSACGHTHGMDLYK 238

RESULT 12
Q8WTC7 PRELIMINARY; PRT; 238 AA.
AC Q8WTC7;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DE 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Green fluorescent protein.
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GN GFP.
OS Aequorea macrodactyla.
OC Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
OC Aequoreidae; Aequorea.
OX NCBI_TaxID=147615;
RN [1]
RA Luo W.X., Zhang J., Yang H.J., Xie X.Y., Li S.W., Guan B.Q., Chen M.,
Li S.J., Xia N.S.;
RT "Colorful mutants of green fluorescent protein from Aequorea
macrodactyla."
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF435430; AAL33915.1; -
DR InterPro; IPR000786; Green_fl_protein.
DR Pfam; PF01353; GFP; 1.
DR ProDom; PD013756; Green_fl_protein; 1.
SQ SEQUENCE 238 AA; 27002 MW; BD5BA2982264C018 CRC64;

Query Match 84.1%; Score 1072; DB 5; Length 238;
Best Local Similarity 81.5%; Pred. No. 9.4e-81;
Matches 194; Conservative 20; Mismatches 24; Indels 0; Gaps 0;

QY 2 VSKGEELFTGVVPIVLVDGVDVNGHKFSVSGEGEDATYKLTGKLFICTTGKLPVWPPTL 61
Db 1 MSKGEELFTGIVPVLIELDGDVGHGKFSVRGEGDADYKLEIKFICTTGKLPVWPPTL 60
QY 62 VTTLSYGVOCSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNKTKRAEVKFGDTLV 121
Db 61 VTTLSYGILCFARYPEHKMNDFFKSAMPEGYIQERTIFFQDDGKYKTRGEVKEGDTLV 120
QY 122 NRIELKGIDFKEDGNILGHKLEYNHNYSVIMADKQNGIKVNFKIRHNIEDGSGVOLAD 181
Db 121 NRIELKGMDFKEDGNILGHKLEYNHNYSVIMADKQNGIKVNFKIRHNIEGGGVQVLAD 180
QY 182 HYQONTPIGDGPVLLPDNHYLSQTALSADKPNKRDHMLVGLGVTAAAGITLGMDELYK 239
Db 181 HYQTNVPLDGPVLLIPINHYLSQTALSKDRNETRDHMLVLEFFSACGHTHGMDLYK 238

RESULT 13
Q8WTC5 PRELIMINARY; PRT; 238 AA.
AC Q8WTC5;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Orange fluorescent protein.
GN GFP.
OS Aequorea macrodactyla.
OC Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
OC Aequoreidae; Aequorea.
OX NCBI_TaxID=147615;
RN [1]
RA Luo W.X., Zhang J., Yang H.J., Xie X.Y., Li S.W., Guan B.Q., Chen M.,
Li S.J., Xia N.S.;
RT "Colorful mutants of green fluorescent protein from Aequorea
macrodactyla."
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF435432; AAL33917.1; -
DR InterPro; IPR000786; Green_fl_protein.
DR Pfam; PF01353; GFP; 1.
DR ProDom; PD013756; Green_fl_protein; 1.
SQ SEQUENCE 238 AA; 75521EA5534E573A CRC64;

Query Match 84.0%; Score 1070; DB 5; Length 238;
Best Local Similarity 82.4%; Pred. No. 1.4e-80;
Matches 196; Conservative 17; Mismatches 25; Indels 0; Gaps 0;

QY 2 VSKGEELFTGVVPIVLVDGVDVNGHKFSVSGEGEDATYKLTGKLFICTTGKLPVWPPTL 61
Db 1 MSKGEELFTGIVPVLIELDGDVGHGKFSVRGEGDADYKLEIKFICTTGKLPVWPPTL 60
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Db 1 MSKGEELFTGVVPIVELDGDVHGKFSVRGEGGDADYKLEIKFICTTGKLPVPWPTL 60
Qy 62 VTTLSYGVCFSRYPDHMKQHDFFKSAPEGVYQVQERTIFFKDDGNKTKRAEVKFEQDTLV 121
Db 61 VTTLSYGILCFARYPEHMKMDFFKSAPEGVYQVQERTIFFKDDGNKTKRAEVKFEQDTLV 120
Qy 122 NRILKGLDFEDGNILGHKLEYNVSHNYIMADKQKNGIKVNFIRHNIEDGVSQVAD 181
Db 121 NRILKGMDFEDGNILGHKLEYNVSHNYIMADKQKNGIKVNFIRHNIEDGVSQVAD 180
Qy 182 HYQNTPIGDGPVLLPDNHYLSTOSALSQKRDHMLVLLGFVTAAGTLGMDLYK 239
Db 181 HYQTNVPLDGPVLLPDNHYLSTOSALSQKRDHMLVLLGFVTAAGTLGMDLYK 238

RESULT 14
Q95UA7 PRELIMINARY; PRT; 225 AA.
AC Q95UA7
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Cyan fluorescent protein (Fragment).
OS Montastraea cavernosa (great star coral).
OC Eukaryota; Metazoa; Chnidaria; Anthozoa; Zoantharia; Scleractinia;
OC Faviina; Faviidae; Montastraea.
OX NCBI_TaxID=63558;
RN [1]
RP SEQUENCE FROM N.A.
RA Falkowski P.G., Sun Y.;
RT "Montastraea cavernosa fluorescent protein.";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY056460; AAL17905.1; -.
DR InterPro; IPR000786; Green_fl_protein.
DR Pfam; PF01353; GFP; 1.
DR ProDom; PD013756; Green_fl_protein; 1.
FT NON_TER
FT 225
SQ SEQUENCE 225 AA; 25775 MW; 52DE2F716D083524 CRC64;

Query Match 19.8%; Score 252.5; DB 5; Length 225;
Best Local Similarity 31.1%; Pred. No. 3.8e-13;
Matches 64; Conservative 43; Mismatches 82; Indels 17; Gaps 7;

Qy 12 VPIVLVDGVDNGHFKFSVSGEGGDATYKGLTKFICTTGKLPVPWPTLVTTLSYGVQ 70
Db 7 VMKILRMDGIVNGHKPMITGEGEGKDPFEGTHTTILKVKEGGPLFPAYDILTTFATQYGNR 66
Qy 71 CFSRYPDHMKQHDFFKSAPEGVYQVQERTIFFKDDGNKTKRAEVKFEQDTLVNRIELKGD 130
Db 67 VTKYKPDIP--DYFKQSFPEGSWSERIMAYEDQSICTATSDIRMEGDCFYEIFYGVN 124
Qy 131 FKEDGNILGHK-LEYNVSHNYIMADKQKNGIKVNFIRHNIEDGVSQVLA-----DHY 183
Db 125 FPGSGPVMQKTKLWEPSTENMTV-----RDGVLGDVSRVTLLEGD---KHRCNFRS 175
Qy 190 GDGP---VLLPDNHYLSTQ-SALSKD 211
Db 176 TYGAKKGVLPEYHFVDHRIEILSHD 201
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RESULT 15
Q963F5 PRELIMINARY; PRT; 225 AA.
AC Q963F5
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Green fluorescent protein.
OS Montastraea cavernosa (great star coral).
OC Eukaryota; Metazoa; Chnidaria; Anthozoa; Zoantharia; Scleractinia;
OC Faviina; Faviidae; Montastraea.
OX NCBI_TaxID=63558;
RN [1]
```

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RP SEQUENCE FROM N.A.
RA Lesser M.P., Barry T.M., Mazel C., Matz M.V., Lukyanov S.A.,
RA Falkowski P., Gorbunov M., Kolber Z.;
RT "Green fluorescent proteins in Caribbean Scleractinian corals.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF384683; AAK62982.2; -.
DR InterPro; IPR000786; Green_fl_protein.
DR Pfam; PF01353; GFP; 1.
DR ProDom; PD013756; Green_fl_protein; 1.
SQ SEQUENCE 225 AA; 25847 MW; 77DE7D7C616929AF CRC64;

Query Match 19.4%; Score 247; DB 5; Length 225;
Best Local Similarity 27.6%; Pred. No. 1.1e-12;
Matches 59; Conservative 42; Mismatches 85; Indels 28; Gaps 6;

Qy 12 VPIVLVDGVDNGHFKFSVSGEGGDATYKGLTKFICTTGKLPVPWPTLVTTLSYGVQ 70
Db 7 IMEIKLRMQGVVNGHFKFVKGEGKPFEGTHTTILTVKEGAPLPFAYDILTSAFQYGNR 66
Qy 71 CFSRYPDHMKQHDFFKSAPEGVYQVQERTIFFKDDGNKTKRAEVKFEQDTLVNRIELKGD 130
Db 67 VTKYKPDIP--DYFKQSFPEGSWSERIMAYEDQSICTATSDIRMEGDCFYEIFYGVN 124
Qy 131 FKEDGNILGHK-LEYNVSHNYIMADKQKNGIKVNFIRHNIEDGVSQVLA-----DHY 183
Db 125 FPGSGPVMQKTKLWEPSTENMTV-----RDGVLGDVSRVTLLEGD---KHRCNFRS 169
Qy 184 Q---QNTPIGDGPVLLPDNHYLSTQSAKSDPNE 214
Db 170 RCDPRSTYKAKKRVQLPDYHFVDHRIEILSHDND 203
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Search completed: June 3, 2003, 15:08:36
Job time : 85 secs